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 Miller, Charles E.  
 Mezes, Peter  
 Hahne, William

<120> COMPOSITIONS AND METHODS OF USE FOR A FIBROBLAST GROWTH FACTOR

<130> Cura-57 SNP

<140> \*\*\*Enter Current Patent Application ID\*\*\*

<141> 2004-11-3

<150> 10/702,126

<151> 2003-11-4

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Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn	85	90	95			
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Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr	100	105	110			
ttc gtt gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct						384
Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser	115	120	125			
aaa cgt cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg						432
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9/19

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10/19

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 165 170 175

cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt 576  
 Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val  
 180 185 190

cca gaa ctg tat aaa aac ctg ctg atg tac acc taa 612  
 Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 15  
 <211> 203  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Gly Phe Leu Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His  
 1 5 10 15

Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg  
 20 25 30

Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln  
 35 40 45

Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg  
 50 55 60

Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr  
 65 70 75 80

Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala  
 85 90 95

Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly  
 100 105 110

Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu  
 115 120 125

Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser

130	135	140	
Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala			
145	150	155	160
Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His			
	165	170	175
Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val			
	180	185	190
Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr			
	195	200	
<210> 16			
<211> 603			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (1)..(600)			
<400> 16			
ggc ggt ctg gag ggt ctg ggt cag cag gtt ggt tct cac ttc ctg ctg			48
Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu			
1	5	10	15
ccg ccg gct ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca			96
Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala			
	20	25	30
gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac			144
Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His			
	35	40	45
ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc			192
Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe			
	50	55	60
cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac			240
His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp			
	65	70	80
cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg			288
His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu			
	85	90	95
gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac			336
Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp			
	100	105	110
aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc			384
Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe			
	115	120	125
cgt gaa cag ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc			432
Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile			
	130	135	140

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tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa 480  
 Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys  
 145 150 155 160

gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc 528  
 Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe  
 165 170 175

acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg 576  
 Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu  
 180 185 190

tat aaa aac ctg ctg atg tac acc taa 603  
 Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

&lt;210&gt; 17

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

Gly Gly Leu Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu  
 1 5 10 15

Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala  
 20 25 30

Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His  
 35 40 45

Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe  
 50 55 60

His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp  
 65 70 75 80

His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu  
 85 90 95

Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp  
 100 105 110

Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe  
 115 120 125

Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile  
 130 135 140

Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys  
 145 150 155 160

Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe  
 165 170 175

Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu  
 180 185 190

Tyr Lys Asn Leu Leu Met Tyr Thr  
 195 200

<210> 18  
 <211> 594  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(591)

<400> 18  
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 Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
 1 5 10 15  
 ggt gaa cgt ccg cca ctg ctg ggt gaa cgt cgc tcc gca gct gaa cgc 96  
 Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg  
 20 25 30  
 tcc gct cgt ggt ggc ccg ggt gct gct cag ctg gct cac ctg cat ggt 144  
 Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
 35 40 45  
 atc ctg cgt cgc cgt cag ctg tac tgc cgt act ggt ttc cac ctg cag 192  
 Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
 50 55 60  
 atc ctg ccg gat ggt tct gtt cag ggt acc cgt cag gac cac tct ctg 240  
 Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
 65 70 75 80  
 ttc ggt atc ctg gaa ttc atc tct gtt gct gtt ggt ctg gtt tct atc 288  
 Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
 85 90 95  
 cgt ggt gtt gac tct ggc ctg tac ctg ggt atg aac gac aaa ggc gaa 336  
 Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
 100 105 110  
 ctg tac ggt tct gaa aaa ctg acc tct gaa tgc atc ttc cgt gaa cag 384  
 Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
 115 120 125  
 ttt gaa gag aac tgg tac aac acc tac tct tcc aac atc tac aaa cat 432  
 Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
 130 135 140  
 ggt gac acc ggc cgt cgc tac ttc gtt gct ctg aac aaa gac ggt acc 480  
 Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
 145 150 155 160  
 ccg cgt gat ggt gct cgt tct aaa cgt cac cag aaa ttc acc cac ttc 528  
 Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
 165 170 175  
 ctg ccg cgc cca gtt gac ccg gag cgt gtt cca gaa ctg tat aaa aac 576  
 Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
 180 185 190  
 ctg ctg atg tac acc taa 594

Leu Leu Met Tyr Thr  
195

<210> 19  
<211> 197  
<212> PRT  
<213> Homo sapiens

<400> 19  
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala  
1 5 10 15  
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg  
20 25 30  
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly  
35 40 45  
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
50 55 60  
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
65 70 75 80  
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
85 90 95  
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
100 105 110  
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
115 120 125  
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
130 135 140  
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
145 150 155 160  
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
165 170 175  
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
180 185 190

Leu Leu Met Tyr Thr  
195

<210> 20  
<211> 567  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(564)

<400> 20  
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His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu



1	5	10	15	
cgt cgc tcc gca gct gaa cgc tcc gct cgt ggt ggc ccg ggt gct gct				96
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala	20	25	30	
cag ctg gct cac ctg cat ggt atc ctg cgt cgc cgt cag ctg tac tgc				144
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys	35	40	45	
cgt act ggt ttc cac ctg cag atc ctg ccg gat ggt tct gtt cag ggt				192
Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly	50	55	60	
acc cgt cag gac cac tct ctg ttc ggt atc ctg gaa ttc atc tct gtt				240
Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val	65	70	75	80
gct gtt ggt ctg gtt tct atc cgt ggt gtt gac tct ggc ctg tac ctg				288
Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu	85	90	95	
ggt atg aac gac aaa ggc gaa ctg tac ggt tct gaa aaa ctg acc tct				336
Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser	100	105	110	
gaa tgc atc ttc cgt gaa cag ttt gaa gag aac tgg tac aac acc tac				384
Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr	115	120	125	
tct tcc aac atc tac aaa cat ggt gac acc ggc cgt cgc tac ttc gtt				432
Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val	130	135	140	
gct ctg aac aaa gac ggt acc ccg cgt gat ggt gct cgt tct aaa cgt				480
Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg	145	150	155	160
cac cag aaa ttc acc cac ttc ctg ccg cgc cca gtt gac ccg gag cgt				528
His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg	165	170	175	
ggt cca gaa ctg tat aaa aac ctg ctg atg tac acc taa				567
Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr	180	185		
<210> 21				
<211> 188				
<212> PRT				
<213> Homo sapiens				
<400> 21				
His Phe Leu Leu Pro Pro Ala Gly Glu Arg Pro Pro Leu Leu Gly Glu	1	5	10	15
Arg Arg Ser Ala Ala Glu Arg Ser Ala Arg Gly Gly Pro Gly Ala Ala	20	25	30	
Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr Cys	35	40	45	

Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly Ser Val Gln Gly  
 50 55 60

Thr Arg Gln Asp His Ser Leu Phe Gly Ile Leu Glu Phe Ile Ser Val  
 65 70 75 80

Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser Gly Leu Tyr Leu  
 85 90 95

Gly Met Asn Asp Lys Gly Glu Leu Tyr Gly Ser Glu Lys Leu Thr Ser  
 100 105 110

Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp Tyr Asn Thr Tyr  
 115 120 125

Ser Ser Asn Ile Tyr Lys His Gly Asp Thr Gly Arg Arg Tyr Phe Val  
 130 135 140

Ala Leu Asn Lys Asp Gly Thr Pro Arg Asp Gly Ala Arg Ser Lys Arg  
 145 150 155 160

His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val Asp Pro Glu Arg  
 165 170 175

Val Pro Glu Leu Tyr Lys Asn Leu Leu Met Tyr Thr  
 180 185

&lt;210&gt; 22

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

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atcctgcgcc gccggcagct ctattgccgc accggcttcc acctgcagat cctgccccgac 60
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gtggcagtgg gactggtcag tattagaggt gtggacagtg gtctctatct tggaatgaat 180
gacaaaggag aactctatgg atcagagaaa cttacttccg aatgcacatt tagggagcag 240
tttgaagaga actggtataa cacctattca tctaacatat ataaacatgg agacactggc 300
cgcaggtatt ttgtggcact taacaaagac ggaactccaa gagatggcgc caggtccaag 360
aggcatcaga aatttacaca tttcttacct agaccagtgg atccagaaaa agttccagaa 420
ttgtacaagg acctactgat gtacact 447

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&lt;210&gt; 23

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln  
 1 5 10 15

Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu  
 20 25 30

Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile  
 35 40 45

Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu  
 50 55 60

Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln  
65 70 75 80

Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His  
85 90 95

Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr  
100 105 110

Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe  
115 120 125

Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asn  
130 135 140

Leu Leu Met Tyr Thr  
145

<210> 24

<211> 537

<212> DNA

<213> Homo sapiens

<400> 24

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agcctcttccg gtatctttgga attcatcagt gtggcagtgg gactggtcag tattagaggt 240
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cttacttccg aatgcatctt tagggagcag tttgaagaga actggtataa cacctattca 360
tctaacatat ataaacatgg agacactggc cgcagggtatt ttgtggcact taacaaagac 420
ggaactccaa gagatggcgc caggtccaag aggcattcaga aatttacaca tttcttacct 480
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